

Appendix A



Consensus #1

BB1193DIVSeqIdNo10
GI 4325324
GenBank X94451

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.....10.....20.....30.....40.....50.....60
LSLHLLRVSPSSPFSRSPPLHNEALVSRDMSGLEEKLAGLSTGGQONPPPAGEGGE 59
ME-----GAADQTTKALSELAMDSSSTLNAAESSAGDGAAGR----- 37
MD-----SSVST 8
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...SKNA.K.E.K.K.E.....E...K.A.....D.TQY..NR
70.....80.....90.....100.....110.....120
PQLSKNAKKREKKKLEKKRRRLKEKKKNKA-AAASGKPQKASAAADDDDMDPTQYYFNR 118
---SKNALKKKEQKMKQKEEBKRRKDBBKAEKAKQAPKASSQKAVAADDEEMDDATQYYFNR 94
P-LSKNAKKREKKKAKEKEQL-----EQEKKAATAVAKRQMEQHNLPLENDLDPPTQYLANR 61
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L.....G.NPYPHKF....S.P.I..Y..L..G.....LAGR...KR.SSS
130.....140.....150.....160.....170.....180
LKALDSLKATGVNPPYPHKFPVGISSVPPRYIEKYYRTLSEGEKLTQVAFCLAGRIMNKR 178
LKYLA AEKAKGENPPYPHKFFAVSMSTPKYIEBTYGSNNGDHVEENAEESLAGRIMSKRS 154
LRNIESLRESGGINPPYPHKFFFITMSTPFFISRYAHLNTGEFFEDIDMSLAGRVISSKRA 121
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KL.FY.L.G....VQV.A.A..S..D...F....S...KRGDI.G..G.PGK..RGELS.F	190	200	210	220	230	240
KLFFYDLYGCGMKVQVMADARTSELDDAEFSKYNHSGVKKRGDIIVGICGYPGKSNRGELSVF	238					
KLFFYDLHGDDFKVQVMADASKGLDDAEFLKLHSHNAKRGDIIVGVIGFPGKTKRGELSVF	214					
KLFFYELGCGARVQVLASARDSDVDAVQPSNYQSGVKKRGDIIVGVRGYPGKSKRGELSVF	181					

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...F..L..CLHM.PR.....W.PG..RN.E.YVL.DQE.RY	250	260	270	280	290	300
PKRFVVLSPCLHMMPRQKGESEAVP-----VPTPGMGRRNIENYVLRDQRRY	286					
PRSFILSHCLHMMPRKADNVNAKKP-----EIMVPGQTNNPBA YV LK DQRRY	263					
AKPFI VLA PCLHMLPRRLTSSIVDETRTQNFQGITAYDTWTTPGDLRNPESYVLRDQRRY	241					

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RQR.LD...N.EVR..F.TR..I.S..R.FLD...FLEVE TP.MN...AGGA.ARPF.THH	310	320	330	340	350	360
RQRYLDLMVNH EVRHIFKTRSKIVSFIRKFLDDR EFL E V E T P M M N M I A G G A A A R P F V T H H	346					
RQRHLDMILNVEVRQIFRTRAKK I I S Y V I R S F L D N K N F L E V E T P M M N M I A G G A A A R P F V T H H	323					
RQRYLDLMMNPEVRALFRTRAR I I S Y I R S F L D N L E F L E V E T P S M N L T A G G A S A R P P I T H H	301					

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GI 4325324
GenBank X94451

motif 1

Appendix A

motif 2

Consensus #1	N . L . . . L . . . R . . . P E L Y L K . L . V G G . R V Y E . G K . F R N E G . D L T H . P E F T . C E . Y M A . A D Y	370	380	390	400	410	420
BB1193DIVSeqIdNo10	N E L N M R L F M R I A P E L Y L K E L V V G G L D R V Y E I G K Q F R N E G I D L T H N P P H F T T C E F Y M A Y A D Y						406
GI 4325324	N D L D M R L Y M R I A P E L Y L K Q L I V G G L E R V Y E I G K Q F R N E G I D L T H N P P H F T T C E F Y M A F A D Y						383
GenBank X94451	N E L D T E L I R V S P E L Y L K K L V V G G F D R V Y E L G K H F R N E G M D L T H S P H F T T C E L Y M A Y A D Y						361
Consensus #1	N D L M . . T E . . L S G M V K . L T G . Y K I . Y . A N G P I E I D F T P P F R . I . M . . . L E . . . A . . .	430	440	450	460	470	480
BB1193DIVSeqIdNo10	N D L M E L T E T M L S G M V K D L T G G Y K I K Y H A N G V T N P P I E I D F T P P P R R I D M T K D L E A M A N L S						466
GI 4325324	N D L M E M T F E V M L S G M V K E L T G G Y K I K Y N A N G Y D K D P I E I D F T P P P R R I E M I G E L E K K V A K L N						443
GenBank X94451	N D L M D L T E Q L L S G M V K D L T G S Y K I R Y H A N G L D N E P I E I D F T P P P R K I D M L S E L E K K V A N I S						421
Consensus #1	I P . D L . S . . A N . . L . . . C . . . D V K C P P P . T T . R L L D K L V G . F . E . . C . N P T F I I N . P E I M	490	500	510	520	530	540
BB1193DIVSeqIdNo10	I P K D L S S D E A N R Y L I E A C V K Y D V K C P P P Q T T S R L L D K L V G H F L E T C V N P P T F I I N E P P I M						526
GI 4325324	I P K D L A S S E F A N K Y L I D A C A R F D V K C P P P Q T T A R L L D K L V G E F L E P T C V N P P T F I I N Q P P I M						503
GenBank X94451	I P R D L S S E S A N K H L V D V Q E K F D V K C P P P H T T T R L L D K L V G H F I E V N C I N P T F I I N H P P I M						481

Appendix A

Consensus #1	SPLAK..RS..GLTERF*LF.N..*E.C.AYTELNDF..QR.RF..QLKDRQ.GDDEAM.L	550560570580590600
BB1193DIVSeqIdNo10	SPLAKWRRSPGLTERRFELFVNKHEV*CNAYTELNDDPVVQRQRFERQQLKDRQSGDDHAAAL	586
GI 4325324	SPLAKWRRSPGLTERRFELFVNKHEV*CNAYTELNDDPVVQRQRFERQQLKDRQSGDDHAAAL	563
GenBank X94451	SPLAKSRSEPGLTERRFELFVNRRHLCDAYTELNDDPTAQRERFAPAEQLKDRQLGDDHAAAL	541
Consensus #1	DE.F..ALEYGL.PTGG.G.GIDRL.MLLTDS.N.KEV..FPPAM.....	610620630640650660
BB1193DIVSeqIdNo10	DETFCTALEYGLAPTGGWGLGIDRLTMLTDSQNIKEVLLPPAMK PQE	634
GI 4325324	DETFCTALEYGLAPTGGWGLGIDRLTMLTDSQNIKEVLLPPAMK PQE	623
GenBank X94451	DETFCTALEYGLAPTGGWGLGIDRLTMLTDSQNIKEVLLPPAMK PQE	588
Consensus #1	...	motif 3
BB1193DIVSeqIdNo10	---	634
GI 4325324	EKK	626
GenBank X94451		588

Consensus #1: When all match the residue on the Consensus show the residue of the Consensus, otherwise show ‘.’

Shade (with black at 40% fill) residues that match the Consensus named “Consensus #1” exactly.

The three highly conserved motifs (1, 2 and 3) are indicated by boxes. Residues which are important for substrate binding are indicated by asterisks.